

Conference Abstract

# Towards FAIR Principles in Biodiversity Research: Enabling computable taxonomic descriptions and ecological data with Phenoscript

Sergei Tarasov<sup>‡</sup>, Giulio Montanaro<sup>‡</sup>, Federica Losacco<sup>‡</sup>, Diego Porto<sup>‡</sup>

<sup>‡</sup> Finnish Museum of Natural History (LUOMUS), Helsinki, Finland

Corresponding author: Sergei Tarasov ([sergei.tarasov@helsinki.fi](mailto:sergei.tarasov@helsinki.fi))

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## Abstract

Taxonomic descriptions hold immense phenotypic data, but their natural language (NL) format poses challenges for computer analysis. In this talk, we will present Phenoscript, a user-friendly computer language enabling computer-readable species descriptions and automated phenotype comparisons, in accordance with FAIR (Findable, Accessible, Interoperable, Reusable) principles.

Phenoscript facilitates the creation of semantic species descriptions that represent a knowledge graph composed of terms from predefined biological ontologies. A Phenoscript description resembles a NL description, but follows a specific language grammar. We have developed the Phenospy package: a Python-based Phenoscript toolkit. Phenospy converts Phenoscript descriptions into both NL format, facilitating scientific publication, and the Web Ontology Language (OWL) format, enabling downstream analysis and computable phenotypic comparisons. OWL is a standard for sharing semantic data on the Web. While initially designed for phenotypes, Phenoscript can be extended to create semantic ecological data, encompassing environmental traits, functional traits, and species interactions. We will discuss the integration of species and ecological traits encoded in Phenoscript into downstream analysis, highlighting its potential for phenomic-level research in biology.

## **Keywords**

semantic description, taxonomy, phenomics, ecology, ontologies, FAIR data

## **Presenting author**

Sergei Tarasov

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## **Conflicts of interest**

The authors have declared that no competing interests exist.